Title :

Q-DNA: A Formal Definition of a Canonical Tetra-Stranded Hereditary Polymer Beyond the Double Helix

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Abstract

DNA's canonical double helix remains the dominant genetic architecture in known biology, yet non-canonical nucleic acid structures—such as G-quadruplexes and i-motifs—demonstrate that nucleic acids can access higher-order multistranded conformations in vitro and in vivo.

In this paper, I introduce **Q-DNA**, defined not as a local quadruplex motif but as a **hereditary polymer whose canonical, genome-scale ground state is tetra-stranded**. I propose a formal axiomatic framework distinguishing Q-DNA from motif-level quadruplexes (e.g., G-quadruplexes) and specify necessary conditions for canonicality, multi-body recognition rules, topologicaladmissibility, and heredity under bounded copying error. I then outline falsifiable predictions and an experimental roadmap leveraging synthetic genetics and XNA technologies, which have already established that alternative genetic polymers can store and propagate information with engineered enzymes.

Keywords: tetra-stranded genome, canonical hereditary state, quadruplex motifs, XNA, synthetic genetics, information theory

1. Introduction

1.1 Motivation: why “tetra-stranded heredity” deserves a formal definition

The double helix described by Watson and Crick provided a structural explanation for heredity and templated replication.

Since then, it has become increasingly clear that nucleic acids occupy a vastconformational landscape. G-quadruplexes are now widely discussed as structurally and functionally relevant motifs, and i-motif structures have been visualized in nuclei of human cells using structure-selective binders.

Yet, almost all modern discussions implicitly treat these multistranded forms as:

- **local** (limited genomic segments),
- **context-dependent** (sequence and environment),
- and typically **embedded** within a largely duplex genome.

I believe the field lacks a precise language to discuss a radically different possibility: **a genetic system where the canonical hereditary state is itself tetra-stranded at genome scale**. This is the conceptual gap I fill with Q-DNA.

1.2 My claim (and what I do not claim)

I claim: there is scientific value in defining a coherent theoretical object—Q-DNA—so that its feasibility can be evaluated with the same rigor used for duplex DNA and synthetic genetic polymers.

I do not claim:

- that Q-DNA exists in extant biology,
- that G-quadruplexes imply Q-DNA,
- or that a single chemical implementation is already established.

Instead, I define **criteria** that any putative Q-DNA system must satisfy and provide **testable predictions.**

2. Prior Art: Multistranded Nucleic Acids Are Not the Same as Canonical Tetra-Heredity

2.1 G-quadruplexes are evidence of multistranded capacity, not of canonical tetra-heredity

G-quadruplexes (G4s) are four-stranded structures formed by guanine-rich sequences and stabilized by specific ionic environments (notably K^+). They are studied for genome regulation and disease contexts.

This matters because it proves that nucleic acids can form **stable multistranded** states in real biochemical settings. However, G4s are still typically treated as **motifs** rather than a global hereditary architecture.

2.2 i-motifs provide a second anchor: four-stranded structures can exist in nuclei

The visualization of i-motif DNA structures in human cell nuclei using an i-motif-selective binder is a strong precedent showing that four-stranded DNA structures can form under physiological conditions.
Again, the key distinction remains: i-motifs are **localized** and **conditional**.

2.3 Synthetic genetics shows that "genetic material" is a design space

The XNA literature establishes that alternative genetic polymers can store information and be replicated or evolved using engineered enzymes, supporting the broader claim that heredity is not chemically unique to DNA/RNA.
This is essential to my argument: Q-DNA can be treated as a system design problem.

3. Formal Definition of Q-DNA

3.1 Core objects and notation

I represent a candidate Q-DNA genome as four strands:

- S_1, S_2, S_3, S_4, each a sequence over an alphabet Σ (canonical bases or synthetic analogs).
- A physical state C_Q that embeds all four strands in a tetra-stranded conformation.
- A state space S of admissible conformations, including duplex-dominant states C_D and motif states C_{motif}.

I emphasize: **Q-DNA is defined at the level of hereditary system behavior**, not merely a structural snapshot.

3.2 Axiom 1 — Canonicality (genome-scale ground-state dominance)

I call a system **Q-DNA** if there exists an environmental domain Ω (ion composition, temperature range, crowding, hydration, etc.) such that **for genome-scale lengths** the tetra-stranded state dominates:

$$G(C_Q \mid \Omega) \leq G(C_D \mid \Omega) - \delta$$

for some margin $\delta > 0$ that persists beyond local motifs.

Interpretation: Q-DNA is not “duplex with occasional quadruplex folding.” It is **tetra-heredity as default**.

3.3 Axiom 2 — Multi-body recognition (beyond pairwise base pairing)

Duplex heredity largely relies on pairwise base pairing (a key conceptual feature of the original duplex model).

In Q-DNA, I require a recognition scheme that is **not reducible** to independent pairwise constraints. I model recognition as a **hypergraph**:

- Nodes: nucleotide positions across strands
- Hyperedges: constraints spanning 3 or **4** nucleotides across strands

This creates an “encoding” where the stable state depends on **collective multi-strand compatibility**, not only pairwise matches.

3.4 Axiom 3 — Topological admissibility (global consistency)

For a genome-scale state, topology is not cosmetic; it determines whether replication, segregation, and repair can be physically well-posed. I therefore require:

- A family of Q-states C_Q exists that is **globally consistent** under long-polymer constraints (no inevitable knots/links that forbid copying/segregation at scale), or that admits an explicit resolution mechanism.

This axiom becomes the foundation for the next paper in the series (classification of Q topologies).

3.5 Axiom 4 — Heredity mapping with bounded copying error

I define heredity as the existence of a replication operator R that maps parent strands to offspring strands:

$$R:(S1,S2,S3,S4)\rightarrow(S1',S2',S3',S4')$$

with an average per-symbol error rate ε that is **bounded below a regime compatible with long sequences**.

I include this axiom because information propagation under noise is a fundamental constraint on any hereditary system, independent of chemistry. (If needed for later papers, I can explicitly formalize this via channel coding language.)

3.6 Axiom 5 — Biochemical plausibility via synthetic genetics (not necessarily natural enzymes)

I do **not** require that extant enzymes replicate Q-DNA. Instead, I require plausible implementability through engineered polymerases or synthetic systems—an assumption consistent with XNA results demonstrating enzyme-enabled replication and information propagation for non-canonical genetic polymers.

4. Operational Exclusion Tests: When Something Is Not Q-DNA

I treat Q-DNA as falsifiable by design. A candidate system is **not** Q-DNA if any of the following hold:

1. **Motif-limited:** tetra-structure forms only in short segments while the genome remains duplex-dominant (typical motif quadruplex behavior).

2. **Environment-fragile:** tetra-state only exists in extremely narrow conditions that cannot support stable heredity across replication cycles.

3. **Recognition reducible:** the encoding reduces to independent base pairs; the tetra-structure is an epiphenomenon.

4. **No heredity operator:** no plausible replicative mapping exists even in principle (with engineered systems).

5. **Topological dead end:** global state implies unavoidable entanglement preventing segregation.

5. Testable Predictions

5.1 Prediction P1: Existence of canonicality windows in environmental space

Because multistranded structures (G4, i-motif) show strong dependence on ions and conditions, I predict Q-DNA candidates will also have stability windows defined by salt/crowding regimes.

Test strategy: design sequences/chemistries; measure relative stability of tetra-state vs duplex/alternatives across Ω.

5.2 Prediction P2: Distinct mechanical signatures at single-molecule level

A genome-scale tetra-state should show distinct force–extension and torque responses compared with duplex DNA.

Test strategy: optical tweezers / magnetic tweezers on designed constructs; compare unfolding/refolding hysteresis.

5.3 Prediction P3: Replication requires characteristic intermediates

Unlike duplex semi-conservative replication, Q-DNA replication should require strand partitioning logic (e.g., 2+2 segregation or stepwise reconstruction).

Test strategy: time-resolved assays (fluorescent strand labeling) once a biochemical replication scheme exists.

5.4 Prediction P4: Multi-body recognition yields different mutational robustness regimes

I predict certain mutation classes will be “absorbed” by multi-strand redundancy (increased robustness), while others will produce correlated failure modes (new fragilities). This can be quantified once a rule set H is chosen.

6. Proposed Figures (with captions)

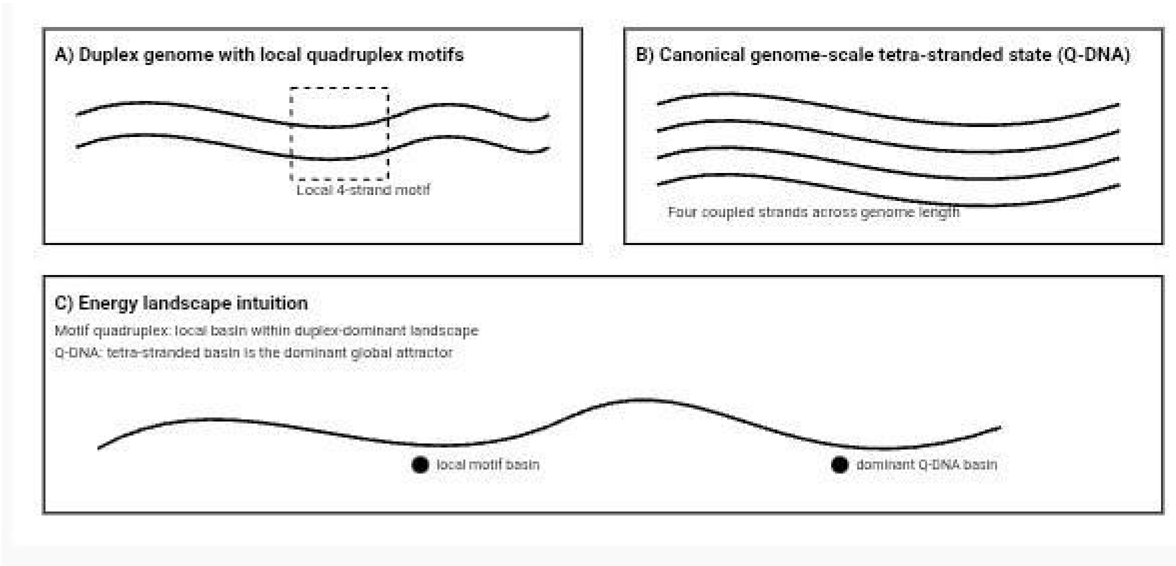

Figure A. “Motif Quadruplexes vs Canonical Q-DNA: A Conceptual Boundary”

Caption: I contrast duplex genomes containing local quadruplex motifs with a genome whose canonical ground state is tetra-stranded. I also sketch an energy landscape: motifs correspond to local basins, while Q-DNA corresponds to the dominant global basin.

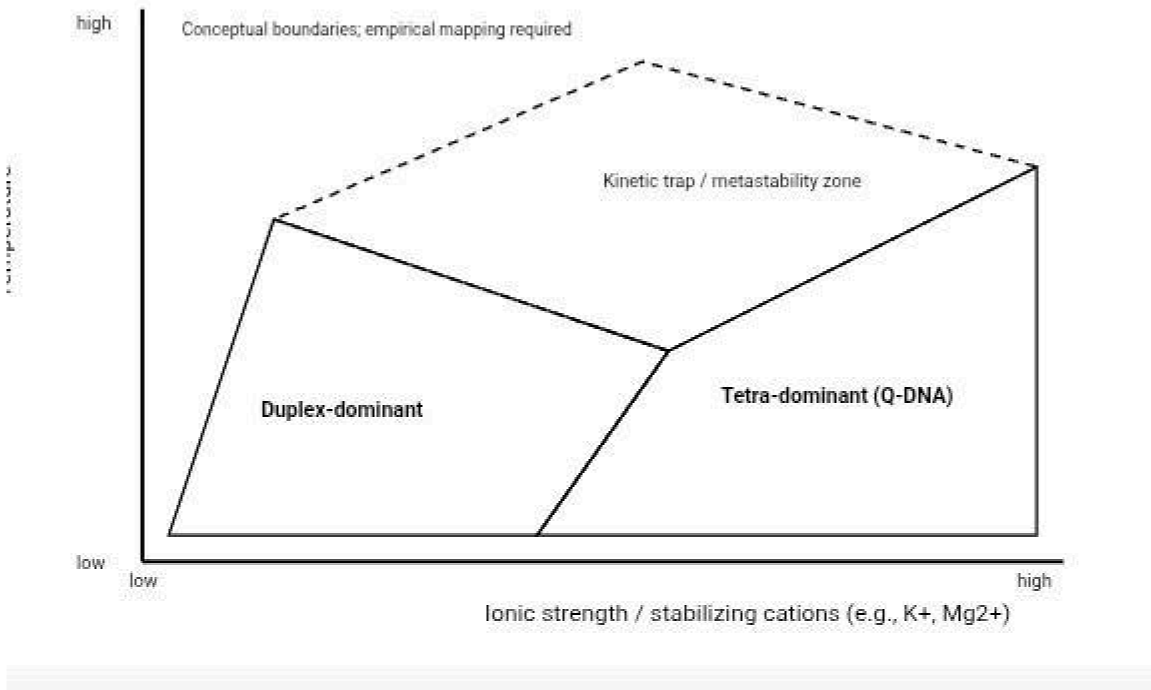

Figure B. “Canonicality Phase Diagram in Environmental Space”

Caption: I show a conceptual phase map (e.g., ionic strength vs temperature) with regions where tetra-state dominates, where duplex dominates, and where kinetics prevents equilibration.

7. Discussion

7.1 Why I insist on "canonicality" (and why motifs are insufficient)

The existence of four-stranded motifs in cells is important evidence that nucleic acids can adopt multistranded states under physiological conditions, as shown by in vivo i-motif visualization and live-cell G4 studies and reviews.

But motif existence does not imply a **global hereditary architecture**. The "canonical" structure must dominate across genome lengths and across replication cycles. This is why Axiom 1 is the cornerstone: it prevents Q-DNA from collapsing into a relabeling of known motif biology.

7.2 The deepest scientific risk: electrostatics and kinetics

A tetra-stranded genome increases backbone charge density and can introduce kinetic traps. Even if a tetra-state is thermodynamically stable for a short motif, genome-scale formation may be kinetically inaccessible without chaperoning or specialized enzymes. I therefore treat canonicality as **thermodynamic + kinetic**: dominance must occur in a physically reachable manner for heredity.

7.3 Why synthetic genetics makes Q-DNA more than philosophy

If heredity were inseparable from DNA's exact chemistry, Q-DNA would be speculation. However, XNA work demonstrates that alternative genetic polymers can store and propagate information with engineered enzymes, reframing heredity as a broader design space.
This does not prove Q-DNA exists—but it makes the proposal scientifically actionable

7.4 What would count as "minimum proof" of Q-DNA?

I propose a minimum proof package:

1. **Structural proof:** reproducible tetra-state as dominant conformation for long constructs under a defined Ω.

2. **Stability proof:** tetra-state persists through simulated replication-like perturbations (thermal/ionic cycling).

3. **Heredity proof (partial):** a demonstrable copying operator for at least one strand subset with bounded error, scalable in principle.

4. **Exclusion proof:** show that the system is not explainable as duplex DNA plus local motifs.

7.5 Scope and limits

This paper is intentionally definitional. It does not attempt to “win” the chemistry problem in one step. Instead, it establishes a clear target so that future work can be cumulative: topology classification, energy models, explicit candidate chemistries, replication schemes, and evolvability simulations.

8. Conclusion

In this paper, I formally define **Q-DNA** as a **canonical, genome-scale tetra-stranded hereditary polymer**, explicitly distinct from local quadruplex motifs such as G-quadruplexes and i-motifs that—while biologically relevant—do not constitute alternative global hereditary ground states.

I provide axioms for canonicality, multi-body recognition, topology, and heredity under bounded copying error, and I outline falsifiable predictions and a feasible research roadmap grounded in synthetic genetics and XNA progress.

By isolating the concept of tetra-stranded heredity from motif-level quadruplex biology, I aim to convert a provocative idea into a precise research object—one that can be tested, refined, or rejected with standard scientific methods.

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